

J. Ford

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/543,407

DATE: 07/09/2001

TIME: 12:43:42

Input Set : A:\406.app.txt

Output Set: N:\CRF3\07092001\I543407.raw

TECH CENTER 1600/2900

AUG 02 2001

1645
RECEIVED

H10

10
8-4-01

ENTERED

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4 <110> APPLICANT: White, Aaron P.
5     Doran, James L.
6     Collinson, S. Karen
7     Kay, William W.
9 <120> TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
10    PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
13 <130> FILE REFERENCE: 920043.406
15 <140> CURRENT APPLICATION NUMBER: US 09/543,407
16 <141> CURRENT FILING DATE: 2000-04-05
18 <160> NUMBER OF SEQ ID NOS: 59
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 456
24 <212> TYPE: DNA
25 <213> ORGANISM: Salmonella enteritidis
27 <400> SEQUENCE: 1
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29 ggcgtcggtc cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc      120
30 ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
31 agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
32 gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
33 gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
34 aataacgccg cgctgggtta tcagaccgca tctgattcca gcgtaatggt gcgtcagggt      420
35 ggttttggca acaacgccac ggctaaccag tattaa      456
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 456
39 <212> TYPE: DNA
40 <213> ORGANISM: Salmonella enteritidis
42 <400> SEQUENCE: 2
43 atgaaaaaca aattgttatt tatgatgttg acaatactgg gtgcgcctgg gattgcaacc      60
44 gcgacaaatt atgatctggc tcgttcagaa tataattttg cggtaaatga attagcaag      120
45 tcttcattta atcaggcggc cattattggt caagtcggca cgataatag tgccagagta      180
46 cgccaggaag gatcaaaact attgtcpgtt atttcacaag aaggaggaaa taatcgggcg      240
47 aaagtcgacc aggcagggaa ttataacttt gcgtatattg agcaaacggg caatgccaac      300
48 gatgccagta tatcgaaag cgcttacggg aatagtcgag ctattatcca gaaaggttct      360
49 ggaaataagg ccaatattac ccagtacggg acgcagaaaa cagcagttgt agtgcagaaa      420
50 cagtcgcata tggctattcg cgtcacccaa cgctaa      456
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 456
54 <212> TYPE: DNA
55 <213> ORGANISM: E. Coli
57 <400> SEQUENCE: 3
58 atgaaacttt taaaagtaga agcaattgca gcaatcgtag tctccggtag cgctctggca      60
59 ggtgttggtc ctacgtacgg cggcggcggt aaccacgggt gtggcggtaa taatagcggc      120
60 ccaaattctg agctgaacat ttaccagtac ggtggcggta actctgcact tgctctgcaa      180
61 actgatgccc gtaactctga cttgactatt acccagcatg gcggcggtaa tgggtcagat      240
62 gttggtcagg gctcagatga cagctcaatc gatctgaccc aacgtggctt cggtaacagc      300

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63 gctactcttg atcagtggaa cggcaaaaat tctgaaatga cggttaaaca gttcgggtgt 360
64 ggcaacggtg ctgcagttga ccagactgca tctaactcct ccgtcaacgt gactcaggtt 420
65 ggctttggta acaacgcgac cgctcatcag tactaa 456
67 <210> SEQ ID NO: 4
68 <211> LENGTH: 456
69 <212> TYPE: DNA
70 <213> ORGANISM: E. Coli
72 <400> SEQUENCE: 4
73 atgaaaaaca aattgttatt tatgatgtta acaatactgg gtg'gcgctgg gattgcagcc 60
74 gcagcaggtt atgatttagc taattcagaa tataacttcg cggtaaataga attgagtaag 120
75 tcttcattta atcaggcagc cataattggt caagctggga ctaataatag tgctcagtta 180
76 cggcagggag gctcaaaact tttggcggtt gttgcgcaag aaggtagtag caaccgggca 240
77 aagattgacc agacaggaga ttataacctt gcatatattg atcaggcggg cagtgcacaac 300
78 gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct 360
79 ggtaataaag caaatattac acagtatggt actcaaaaaa cggcaattgt agtgcagaga 420
80 cagtcgcaaa tggctattcg cgtgacacaa cgtaa 456
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 151
84 <212> TYPE: PRT
85 <213> ORGANISM: Salmonella enteritidis
87 <400> SEQUENCE: 5
88 Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
89 1 5 10 15
90 Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
91 20 25 30
92 Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
93 35 40 45
94 Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
95 50 55 60
96 Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
97 65 70 75 80
98 Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
99 85 90 95
100 Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
101 100 105 110
102 Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
103 115 120 125
104 Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
105 130 135 140
106 Asn Ala Thr Ala Asn Gln Tyr
107 145 150
109 <210> SEQ ID NO: 6
110 <211> LENGTH: 151
111 <212> TYPE: PRT
112 <213> ORGANISM: Salmonella enteritidis
114 <400> SEQUENCE: 6
115 Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
116 1 5 10 15
117 Gly Ile Ala Thr Ala Thr Asn Tyr Asp Leu Ala Arg Ser Glu Tyr Asn

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118          20          25          30
119 Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
120          35          40          45
121 Ile Gly Gln Val Gly Thr Asp Asn Ser Ala Arg Val Arg Gln Glu Gly
122          50          55          60
123 Ser Lys Leu Leu Ser Val Ile Ser Gln Glu Gly Gly Asn Asn Arg Ala
124 65          70          75          80
125 Lys Val Asp Gln Ala Gly Asn Tyr Asn Phe Ala Tyr Ile Glu Gln Thr
126          85          90          95
127 Gly Asn Ala Asn Asp Ala Ser Ile Ser Gln Ser Ala Tyr Gly Asn Ser
128          100          105          110
129 Ala Ala Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
130          115          120          125
131 Tyr Gly Thr Gln Lys Thr Ala Val Val Val Gln Lys Gln Ser His Met
132          130          135          140
133 Ala Ile Arg Val Thr Gln Arg
134 145          150
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 151
138 <212> TYPE: PRT
139 <213> ORGANISM: Escherichia coli
141 <400> SEQUENCE: 7
142 Met Lys Leu Leu Lys Val Ala Ala Ile Ala Ala Ile Val Phe Ser Gly
143 1          5          10          15
144 Ser Ala Leu Ala Gly Val Val Pro Gln Tyr Gly Gly Gly Gly Asn His
145          20          25          30
146 Gly Gly Gly Gly Asn Asn Ser Gly Pro Asn Ser Glu Leu Asn Ile Tyr
147          35          40          45
148 Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala Leu Gln Thr Asp Ala Arg
149          50          55          60
150 Asn Ser Asp Leu Thr Ile Thr Gln His Gly Gly Gly Asn Gly Ala Asp
151 65          70          75          80
152 Val Gly Gln Gly Ser Asp Asp Ser Ser Ile Asp Leu Thr Gln Arg Gly
153          85          90          95
154 Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp Asn Gly Lys Asn Ser Glu
155          100          105          110
156 Met Thr Val Lys Gln Phe Gly Gly Gly Asn Gly Ala Ala Val Asp Gln
157          115          120          125
158 Thr Ala Ser Asn Ser Ser Val Asn Val Thr Gln Val Gly Phe Gly Asn
159          130          135          140
160 Asn Ala Thr Ala His Gln Tyr
161 145          150
163 <210> SEQ ID NO: 8
164 <211> LENGTH: 151
165 <212> TYPE: PRT
166 <213> ORGANISM: Escherichia coli
168 <400> SEQUENCE: 8
169 Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
170 1          5          10          15

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```

171 Gly Ile Ala Ala Ala Ala Gly Tyr Asp Leu Ala Asn Ser Glu Tyr Asn
172          20          25          30
173 Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
174          35          40          45
175 Ile Gly Gln Ala Gly Thr Asn Asn Ser Ala Gln Leu Arg Gln Gly Gly
176          50          55          60
177 Ser Lys Leu Leu Ala Val Val Ala Gln Glu Gly Ser Ser Asn Arg Ala
178 65          70          75          80
179 Lys Ile Asp Gln Thr Gly Asp Tyr Asn Leu Ala Tyr Ile Asp Gln Ala
180          85          90          95
181 Gly Ser Ala Asn Asp Ala Ser Ile Ser Gln Gly Ala Tyr Gly Asn Thr
182          100          105          110
183 Ala Met Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
184          115          120          125
185 Tyr Gly Thr Gln Lys Thr Ala Ile Val Val Gln Arg Gln Ser Gln Met
186          130          135          140
187 Ala Ile Arg Val Thr Gln Arg
188 145          150
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 48
192 <212> TYPE: DNA
193 <213> ORGANISM: Leishmania major
195 <400> SEQUENCE: 9
196 tatgatcagc tgggttaccgc tggtgttacc catgaaatgg cacatgca      48
198 <210> SEQ ID NO: 10
199 <211> LENGTH: 16
200 <212> TYPE: PRT
201 <213> ORGANISM: Leishmania major
203 <400> SEQUENCE: 10
204 Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala
205 1          5          10          15
207 <210> SEQ ID NO: 11
208 <211> LENGTH: 456
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
214     sequence containing the replacement fragment
215     encoding PT3 from GP63 of Leishmania major.
217 <400> SEQUENCE: 11
218 atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
219 ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc      120
220 ccggactcaa cggttagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
221 agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
222 gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
223 gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
224 aataacgccg cgctgggttaa ttatgatcag ctggttaccc gtgttggtac ccatgaaatg      420
225 gcacatgcaa acaacgccac ggctaaccag tattaa      456
227 <210> SEQ ID NO: 12

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228 <211> LENGTH: 151
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
234     sequence containing the replacement fragment
235     encoding PT3 from GP63 of Leishmania major.
237 <400> SEQUENCE: 12
238 Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
239   1           5           10           15
240 Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
241           20           25           30
242 Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
243           35           40           45
244 Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
245           50           55           60
246 Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
247 65           70           75           80
248 Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
249           85           90           95
250 Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
251           100          105          110
252 Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Tyr
253           115          120          125
254 Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn
255           130          135          140
256 Asn Ala Thr Ala Asn Gln Tyr
257 145          150
259 <210> SEQ ID NO: 13
260 <211> LENGTH: 456
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
266     sequence containing the replacement fragment
267     encoding PT3 from GP63 of Leishmania major..
269 <400> SEQUENCE: 13
270 atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
271 ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcgcaa tagttccggc      120
272 ccgactcaa cggtgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
273 agcgatgcc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
274 gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
275 gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atatgatcag      360
276 ctggttaccc gtgttggttac ccatgaaatg gcacatgcaa gcgtaatggt gcgtcagggt      420
277 ggttttggca acaacgccac ggctaaccag tattaa      456
279 <210> SEQ ID NO: 14
280 <211> LENGTH: 151
281 <212> TYPE: PRT
282 <213> ORGANISM: Artificial Sequence

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 Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33

L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33

L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59

L:1149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59